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SEQUENCE LISTING

<110> AGO, HIDEO
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ADACHI, TSUYOSHI

<120> HCV POLYMERASE SUITABLE FOR CRYSTAL STRUCTURE ANALYSIS
AND METHOD FOR USING THE ENZYME

<130> 09299.0002-00000

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<150> JP 11-188630
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<150> JP 11-192488
<151> 1999-07-07

<160> 28

<170> PatentIn Ver. 2.1

<210> 1
<211> 591
<212> PRT
<213> Hepatitis C virus

<400> 1
Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Ala Ala
1 5 10 15
Glu Glu Ser Lys Leu Pro Ile Asn Ala Leu Ser Asn Ser Leu Leu Arg
20 25 30
His His Asn Met Val Tyr Ala Thr Thr Ser Arg Ser Ala Gly Leu Arg
35 40 45
Gln Lys Lys Val Thr Phe Asp Arg Leu Gln Val Leu Asp Asp His Tyr
50 55 60
Arg Asp Val Leu Lys Glu Met Lys Ala Lys Ala Ser Thr Val Lys Ala
65 70 75 80
Lys Leu Leu Ser Val Glu Glu Ala Cys Lys Leu Thr Pro Pro His Ser
85 90 95
Ala Lys Ser Lys Phe Gly Tyr Gly Ala Lys Asp Val Arg Asn Leu Ser
100 105 110
Ser Lys Ala Val Asn His Ile His Ser Val Trp Lys Asp Leu Leu Glu
115 120 125

Asp Thr Val Thr Pro Ile Asp Thr Thr Ile Met Ala Lys Asn Glu Val
 130 135 140

Phe Cys Val Gln Pro Glu Lys Gly Gly Arg Lys Pro Ala Arg Leu Ile
 145 150 155 160

Val Phe Pro Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu Tyr
 165 170 175

Asp Val Val Ser Thr Leu Pro Gln Val Val Met Gly Ser Ser Tyr Gly
 180 185 190

Phe Gln Tyr Ser Pro Gly Gln Arg Val Glu Phe Leu Val Asn Thr Trp
 195 200 205

Lys Ser Lys Lys Asn Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys Phe
 210 215 220

Asp Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr
 225 230 235 240

Gln Cys Cys Asp Leu Ala Pro Glu Ala Arg Gln Ala Ile Lys Ser Leu
 245 250 255

Thr Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln
 260 265 270

Asn Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser
 275 280 285

Cys Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Cys Arg
 290 295 300

Ala Ala Lys Leu Gln Asp Cys Thr Met Leu Val Asn Gly Asp Asp Leu
 305 310 315 320

Val Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala Ala Ser Leu
 325 330 335

Arg Val Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly Asp
 340 345 350

Pro Pro Gln Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser Ser
 355 360 365

Asn Val Ser Val Ala His Asp Ala Ser Gly Lys Arg Val Tyr Tyr Leu
 370 375 380

Thr Arg Asp Pro Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr Ala
 385 390 395 400

Arg His Thr Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Met Tyr Ala
 405 410 415

Pro Thr Leu Trp Ala Arg Met Ile Leu Met Thr His Phe Phe Ser Ile
 420 425 430

Leu Leu Ala Gln Glu Gln Leu Glu Lys Ala Leu Asp Cys Gln Ile Tyr
 435 440 445

Gly Ala Cys Tyr Ser Ile Glu Pro Leu Asp Leu Pro Gln Ile Ile Glu
 450 455 460

Arg Leu His Gly Leu Ser Ala Phe Ser Leu His Ser Tyr Ser Pro Gly
 465 470 475 480

Glu Ile Asn Arg Val Ala Ser Cys Leu Arg Lys Leu Gly Val Pro Pro
 485 490 495

Leu Arg Val Trp Arg His Arg Ala Arg Ser Val Arg Ala Arg Leu Leu
 500 505 510

Ser Gln Gly Gly Arg Ala Ala Thr Cys Gly Lys Tyr Leu Phe Asn Trp
 515 520 525

Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Ile Pro Ala Ala Ser Gln
 530 535 540

Leu Asp Leu Ser Gly Trp Phe Val Ala Gly Tyr Ser Gly Gly Asp Ile
 545 550 555 560

Tyr His Ser Leu Ser Arg Ala Arg Pro Arg Trp Phe Met Leu Cys Leu
 565 570 575

Leu Leu Leu Ser Val Gly Val Ile Tyr Leu Leu Pro Asn Arg
 580 585 590

<210> 2
 <211> 1743
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: DNA encoding
 fusion protein consisting of a portion of HCV
 polymerase and histidine tag at the C-terminus

<220>
 <221> CDS
 <222> (1)..(1743)

<400> 2
 atg tca atg tcc tac aca tgg aca ggc gcc ttg atc acg cca tgc gct 48
 Met Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Ala
 1 5 10 15

gag gag gaa agc aag ctg ccc atc aac gcg ttg agc aac tct ttg ctg Ala Glu Glu Ser Lys Leu Pro Ile Asn Ala Leu Ser Asn Ser Leu Leu	96
20 25 30	
cgc cac cat aac atg gtt tat gcc aca aca tct cgc agc gca ggc ctg Arg His His Asn Met Val Tyr Ala Thr Thr Ser Arg Ser Ala Gly Leu	144
35 40 45	
cgg cag aag aag gtc acc ttt gac aga ctg caa gtc ctg gac gac cac Arg Gln Lys Lys Val Thr Phe Asp Arg Leu Gln Val Leu Asp Asp His	192
50 55 60	
tac cggtt gac gtc aag gag atg aag gcg aag gcg tcc aca gtt aag Tyr Arg Asp Val Leu Lys Glu Met Lys Ala Lys Ala Ser Thr Val Lys	240
65 70 75 80	
gct aaa ctc cta tcc gta gag gaa gcc tgc aag ctg acg ccc cca cat Ala Lys Leu Leu Ser Val Glu Glu Ala Cys Lys Leu Thr Pro Pro His	288
85 90 95	
tcg gcc aaa tcc aag ttt ggc tat ggg gca aag gac gtc cgg aac cta Ser Ala Lys Ser Lys Phe Gly Tyr Gly Ala Lys Asp Val Arg Asn Leu	336
100 105 110	
tcc agc aag gcc gtt aac cac atc cac tcc gtg tgg aag gac ttg ctg Ser Ser Lys Ala Val Asn His Ile His Ser Val Trp Lys Asp Leu Leu	384
115 120 125	
gaa gac act gtg aca cca att gac acc acc atc atg gca aaa aat gag Glu Asp Thr Val Thr Pro Ile Asp Thr Thr Ile Met Ala Lys Asn Glu	432
130 135 140	
gtt ttc tgt gtc caa cca gag aaa gga ggc cgt aag cca gcc cgc ctt Val Phe Cys Val Gln Pro Glu Lys Gly Arg Lys Pro Ala Arg Leu	480
145 150 155 160	
atc gta ttc cca gat ctg gga gtc cgt gta tgc gag aag atg gcc ctc Ile Val Phe Pro Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu	528
165 170 175	
tat gat gtg gtc tcc acc ctt cct cag gtc gtg atg ggc tcc tca tac Tyr Asp Val Val Ser Thr Leu Pro Gln Val Val Met Gly Ser Ser Tyr	576
180 185 190	
gga ttc cag tac tct cct ggg cag cga gtc gag ttc ctg gtg aat acc Gly Phe Gln Tyr Ser Pro Gly Gln Arg Val Glu Phe Leu Val Asn Thr	624
195 200 205	
tgg aaa tca aag aaa aac ccc atg ggc ttt tca tat gac act cgc tgt Trp Lys Ser Lys Lys Asn Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys	672
210 215 220	

ttc gac tca acg gtc acc gag aac gac atc cgt gtt gag gag tca att Phe Asp Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile 225 230 235 240	720
tac caa tgt tgt gac ttg gcc ccc gaa gcc aga cag gcc ata aaa tcg Tyr Gln Cys Cys Asp Leu Ala Pro Glu Ala Arg Gln Ala Ile Lys Ser 245 250 255	768
ctc aca gag cgg ctt tat atc ggg ggt cct ctg act aat tca aaa ggg Leu Thr Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly 260 265 270	816
cag aac tgc ggt tat cgc cgg tgc cgc gcg agc ggc gtg ctg acg act Gln Asn Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr 275 280 285	864
agc tgc ggt aac acc ctc aca tgt tac ttg aag gcc tct gca gcc tgt Ser Cys Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Cys 290 295 300	912
cga gct gcg aag ctc cag gac tgc acg atg ctc gtg aac gga gac gac Arg Ala Ala Lys Leu Gln Asp Cys Thr Met Leu Val Asn Gly Asp Asp 305 310 315 320	960
ctc gtc gtt atc tgt gaa agc gcg gga acc caa gag gac gcg gcg agc Leu Val Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala Ala Ser 325 330 335	1008
cta cga gtc ttc acg gag gct atg act agg tac tcc gcc ccc ccc ggg Leu Arg Val Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly 340 345 350	1056
gac ccg ccc caa cca gaa tac gac ttg gag ctg ata aca tca tgt tcc Asp Pro Pro Gln Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser 355 360 365	1104
tcc aat gtg tcg gtc gcc cac gat gca tca ggc aaa agg gtg tac tac Ser Asn Val Ser Val Ala His Asp Ala Ser Gly Lys Arg Val Tyr Tyr 370 375 380	1152
ctc acc cgt gat ccc acc acc ccc ctc gca cgg gct gcg tgg gag aca Leu Thr Arg Asp Pro Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr 385 390 395 400	1200
gct aga cac act cca gtt aac tcc tgg cta ggc aac att att atg tat Ala Arg His Thr Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Met Tyr 405 410 415	1248
gcg ccc act ttg tgg gca agg atg att ctg atg act cac ttc ttc tcc Ala Pro Thr Leu Trp Ala Arg Met Ile Leu Met Thr His Phe Phe Ser 420 425 430	1296

atc ctt cta gcg cag gag caa ctt gaa aaa gcc ctg gac tgc cag atc Ile Leu Leu Ala Gln Glu Gln Leu Glu Lys Ala Leu Asp Cys Gln Ile 435 440 445	1344
tac ggg gcc tgt tac tcc att gag cca ctt gac cta cct cag atc att Tyr Gly Ala Cys Tyr Ser Ile Glu Pro Leu Asp Leu Pro Gln Ile Ile 450 455 460	1392
gaa cga ctc cat ggc ctt agc gca ttt tca ctc cat agt tac tct cca Glu Arg Leu His Gly Leu Ser Ala Phe Ser Leu His Ser Tyr Ser Pro 465 470 475 480	1440
ggg gag atc aat agg gtg gct tca tgc ctc agg aaa ctt ggg gta cca Gly Glu Ile Asn Arg Val Ala Ser Cys Leu Arg Lys Leu Gly Val Pro 485 490 495	1488
ccc ttg cga gtc tgg aga cat cgg gcc agg agc gtc cgc gct agg cta Pro Leu Arg Val Trp Arg His Arg Ala Arg Ser Val Arg Ala Arg Leu 500 505 510	1536
ctg tcc cag ggg ggg agg gcc act tgt ggc aag tac ctc ttc aac Leu Ser Gln Gly Arg Ala Ala Thr Cys Gly Lys Tyr Leu Phe Asn 515 520 525	1584
tgg gca gtg aag acc aaa ctc aaa ctc act cca atc ccg gct gcg tcc Trp Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Ile Pro Ala Ala Ser 530 535 540	1632
cag ctg gac ttg tcc ggc tgg ttc gtt gct ggt tac agc ggg gga gac Gln Leu Asp Leu Ser Gly Trp Phe Val Ala Gly Tyr Ser Gly Gly Asp 545 550 555 560	1680
ata tat cac agc ctg tct cgt gcc cga ccc cgc gga tcc cat cac cat Ile Tyr His Ser Leu Ser Arg Ala Arg Pro Arg Gly Ser His His His 565 570 575	1728
cac cat cac taa taa His His His	1743

<210> 3
<211> 579
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion protein
consisting of a portion of HCV polymerase and
histidine tag at the C-terminus

<400> 3
Met Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Ala
1 5 10 15

Ala Glu Glu Ser Lys Leu Pro Ile Asn Ala Leu Ser Asn Ser Leu Leu
 20 25 30

Arg His His Asn Met Val Tyr Ala Thr Thr Ser Arg Ser Ala Gly Leu
 35 40 45

Arg Gln Lys Lys Val Thr Phe Asp Arg Leu Gln Val Leu Asp Asp His
 50 55 60

Tyr Arg Asp Val Leu Lys Glu Met Lys Ala Lys Ala Ser Thr Val Lys
 65 70 75 80

Ala Lys Leu Leu Ser Val Glu Glu Ala Cys Lys Leu Thr Pro Pro His
 85 90 95

Ser Ala Lys Ser Lys Phe Gly Tyr Gly Ala Lys Asp Val Arg Asn Leu
 100 105 110

Ser Ser Lys Ala Val Asn His Ile His Ser Val Trp Lys Asp Leu Leu
 115 120 125

Glu Asp Thr Val Thr Pro Ile Asp Thr Thr Ile Met Ala Lys Asn Glu
 130 135 140

Val Phe Cys Val Gln Pro Glu Lys Gly Gly Arg Lys Pro Ala Arg Leu
 145 150 155 160

Ile Val Phe Pro Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu
 165 170 175

Tyr Asp Val Val Ser Thr Leu Pro Gln Val Val Met Gly Ser Ser Tyr
 180 185 190

Gly Phe Gln Tyr Ser Pro Gly Gln Arg Val Glu Phe Leu Val Asn Thr
 195 200 205

Trp Lys Ser Lys Lys Asn Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys
 210 215 220

Phe Asp Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile
 225 230 235 240

Tyr Gln Cys Cys Asp Leu Ala Pro Glu Ala Arg Gln Ala Ile Lys Ser
 245 250 255

Leu Thr Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly
 260 265 270

Gln Asn Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr
 275 280 285

Ser Cys Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Cys
 290 295 300

Arg Ala Ala Lys Leu Gln Asp Cys Thr Met Leu Val Asn Gly Asp Asp
 305 310 315 320

Leu Val Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala Ala Ser
 325 330 335

Leu Arg Val Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly
 340 345 350

Asp Pro Pro Gln Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser
 355 360 365

Ser Asn Val Ser Val Ala His Asp Ala Ser Gly Lys Arg Val Tyr Tyr
 370 375 380

Leu Thr Arg Asp Pro Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr
 385 390 395 400

Ala Arg His Thr Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Met Tyr
 405 410 415

Ala Pro Thr Leu Trp Ala Arg Met Ile Leu Met Thr His Phe Phe Ser
 420 425 430

Ile Leu Leu Ala Gln Glu Gln Leu Glu Lys Ala Leu Asp Cys Gln Ile
 435 440 445

Tyr Gly Ala Cys Tyr Ser Ile Glu Pro Leu Asp Leu Pro Gln Ile Ile
 450 455 460

Glu Arg Leu His Gly Leu Ser Ala Phe Ser Leu His Ser Tyr Ser Pro
 465 470 475 480

Gly Glu Ile Asn Arg Val Ala Ser Cys Leu Arg Lys Leu Gly Val Pro
 485 490 495

Pro Leu Arg Val Trp Arg His Arg Ala Arg Ser Val Arg Ala Arg Leu
 500 505 510

Leu Ser Gln Gly Gly Arg Ala Ala Thr Cys Gly Lys Tyr Leu Phe Asn
 515 520 525

Trp Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Ile Pro Ala Ala Ser
 530 535 540

Gln Leu Asp Leu Ser Gly Trp Phe Val Ala Gly Tyr Ser Gly Gly Asp
 545 550 555 560

Ile Tyr His Ser Leu Ser Arg Ala Arg Pro Arg Gly Ser His His His
 565 570 575

His His His

<210> 4
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer, 5BNdelFW

<220>
<221> primer_bind
<222> (1)..(30)

<400> 4
catatgtcaa tgtcctacac atggacagcc

30

<210> 5
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer, 5B570HRV

<220>
<221> primer_bind
<222> (1)..(57)

<400> 5
ttattagtga tggtgatggatggatcc gcggggatcgatgcacgagaca ggctgtg

57

<210> 6
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer, 5B552HRV

<220>
<221> primer_bind
<222> (1)..(57)

<400> 6
ttattagtga tggtgatggatcc aacgaaccagg ccggacaagt ccagctg

57

<210> 7
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer, 5B544HRV

<220>
<221> primer_bind
<222> (1)..(57)

<400> 7
ttattagtga tggatggatgtt gatggatcc ctgggacgca gccggattt gagtgag 57

<210> 8
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer, 5B536HRV

<220>
<221> primer_bind
<222> (1)..(67)

<400> 8
ttattagtga tggatggatgtt gatggatcc gagttttagt ttggctttca ctgcccgattt 60
gaagagg 67

<210> 9
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer, 5B531HRV

<220>
<221> primer_bind
<222> (1)..(60)

<400> 9
ttattagtga tggatggatgtt gatggatcc cttcactgcc cagttgaaga ggtacttgcc 60

<210> 10
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer, 5B591HRV

<220>
<221> primer_bind
<222> (1)..(52)

<400> 10 ttattaaatgg tcatgggtgat ggtgtccgga tcgattgggg agcaggtaga tg 52

<210> 11
<211> 9
<212> PRT
<213> Hepatitis C virus

<220>
<221> MOD_RES
<222> (1)..(3)
<223> Variable amino acid or not present

<220>
<221> MOD_RES
<222> (5)..(6)
<223> Variable amino acid

<220>
<221> MOD_RES
<222> (9)
<223> Variable amino acid or not present

<400> 11
Xaa Xaa Xaa Leu Xaa Xaa Trp Phe Xaa
1 5

<210> 12
<211> 8
<212> PRT
<213> Hepatitis C virus

<400> 12
Lys Asp Leu Ser Gly Trp Phe Lys
1 5

<210> 13
<211> 9
<212> PRT
<213> Hepatitis C virus

<400> 13
Lys Lys Asp Leu Ser Gly Trp Phe Lys
1 5

<210> 14
<211> 8
<212> PRT
<213> Hepatitis C virus

<400> 14
Lys Asp Leu Ser Gly Trp Phe Val
1 5

<210> 15
<211> 8
<212> PRT
<213> Hepatitis C virus

<400> 15
Leu Asp Leu Ser Gly Trp Phe Lys
1 5

<210> 16
<211> 8
<212> PRT
<213> Hepatitis C virus

<400> 16
Leu Asp Leu Ser Gly Trp Phe Val
1 5

<210> 17
<211> 7
<212> PRT
<213> Hepatitis C virus

<400> 17
Asp Leu Ser Gly Trp Phe Val
1 5

<210> 18
<211> 6
<212> PRT
<213> Hepatitis C virus

<400> 18
Asp Leu Ser Gly Trp Phe
1 5

<210> 19
<211> 6
<212> PRT
<213> Hepatitis C virus

<400> 19
Leu Ser Gly Trp Phe Val
1 5

<210> 20
<211> 5
<212> PRT
<213> Hepatitis C virus

<400> 20
Leu Ser Gly Trp Phe
1 5

<210> 21
<211> 6
<212> PRT
<213> Hepatitis C virus

<400> 21
Leu Ser Gly Trp Phe Lys
1 5

<210> 22
<211> 6
<212> PRT
<213> Hepatitis C virus

<400> 22
Lys Leu Ser Gly Trp Phe
1 5

<210> 23
<211> 5
<212> PRT
<213> Hepatitis C virus

<400> 23
Leu Gly Gly Trp Phe
1 5

<210> 24
<211> 5
<212> PRT
<213> Hepatitis C virus

<400> 24
Leu Ser Asp Trp Phe
1 5

<210> 25
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 25
Gly Ser His His Asp His His His
1 5

<210> 26
<211> 578
<212> PRT
<213> Hepatitis C virus

<400> 26
Ser Met Ser Phe Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Ala Ala
1 5 10 15

Glu Glu Ser Lys Leu Pro Ile Asn Ala Leu Ser Asn Ser Leu Leu Arg
20 25 30

His His Asn Met Val Tyr Ala Thr Thr Ser Arg Ser Ala Gly Leu Arg
35 40 45

Gln Lys Lys Val Thr Phe Asp Arg Leu Gln Val Leu Asp Asp His Tyr
50 55 60

Arg Asp Val Leu Lys Glu Met Lys Ala Lys Ala Ser Thr Val Lys Ala
65 70 75 80

Lys Leu Leu Ser Val Glu Glu Ala Cys Lys Leu Thr Pro Pro His Ser
85 90 95

Ala Lys Ser Lys Phe Gly Tyr Gly Ala Lys Asp Val Arg Asn Leu Ser
100 105 110

Ser Lys Ala Val Asn His Ile His Ser Val Trp Lys Asp Leu Leu Glu
 115 120 125

Asp Thr Val Thr Pro Ile Asp Thr Thr Ile Met Ala Lys Asn Glu Val
 130 135 140

Phe Cys Val Gln Pro Glu Lys Gly Gly Arg Lys Pro Ala Arg Leu Ile
 145 150 155 160

Val Phe Pro Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu Tyr
 165 170 175

Asp Val Val Ser Thr Leu Pro Gln Val Val Met Gly Ser Ser Tyr Gly
 180 185 190

Phe Gln Tyr Ser Pro Gly Gln Arg Val Glu Phe Leu Val Asn Thr Trp
 195 200 205

Lys Ser Lys Lys Asn Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys Phe
 210 215 220

Asp Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr
 225 230 235 240

Gln Cys Cys Asp Leu Ala Pro Glu Ala Arg Gln Ala Ile Lys Ser Leu
 245 250 255

Thr Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln
 260 265 270

Asn Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser
 275 280 285

Cys Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Cys Arg
 290 295 300

Ala Ala Lys Leu Gln Asp Cys Thr Met Leu Val Asn Gly Asp Asp Leu
 305 310 315 320

Val Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala Ala Ser Leu
 325 330 335

Arg Val Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly Asp
 340 345 350

Pro Pro Gln Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser Ser
 355 360 365

Asn Val Ser Val Ala His Asp Ala Ser Gly Lys Arg Val Tyr Tyr Lys
 370 375 380

Thr Arg Asp Pro Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr Ala
 385 390 395 400

Arg His Thr Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Met Tyr Ala
 405 410 415

 Pro Thr Leu Trp Ala Arg Met Ile Leu Met Thr His Phe Phe Ser Ile
 420 425 430

 Leu Leu Ala Gln Glu Gln Leu Glu Lys Ala Leu Asp Cys Gln Ile Tyr
 435 440 445

 Gly Ala Cys Tyr Ser Ile Glu Pro Leu Asp Leu Pro Gln Ile Ile Glu
 450 455 460

 Arg Leu His Gly Leu Ser Ala Phe Ser Leu His Ser Tyr Ser Pro Gly
 465 470 475 480

 Glu Ile Asn Arg Val Ala Ser Cys Leu Arg Lys Leu Gly Val Pro Pro
 485 490 495

 Leu Arg Val Trp Arg His Arg Ala Arg Ser Val Arg Ala Arg Leu Leu
 500 505 510

 Ser Gln Gly Gly Arg Ala Ala Thr Cys Gly Lys Tyr Leu Phe Asn Trp
 515 520 525

 Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Ile Pro Ala Ala Ser Arg
 530 535 540

 Leu Asp Leu Ser Gly Trp Phe Val Ala Gly Tyr Ser Gly Gly Asp Ile
 545 550 555 560

 Tyr His Ser Leu Ser Arg Ala Arg Pro Arg Gly Ser His His His His
 565 570 575

 His His

<210> 27
 <211> 465
 <212> PRT
 <213> Human poliovirus 1

<400> 27
 Met Arg Pro Ser Lys Glu Val Gly Tyr Pro Ile Ile Asn Ala Pro Ser
 1 5 10 15

 Lys Thr Lys Leu Glu Pro Ser Ala Phe His Tyr Val Phe Glu Gly Val
 20 25 30

 Lys Glu Pro Ala Val Leu Thr Lys Asn Asp Pro Arg Leu Lys Thr Asp
 35 40 45

 Phe Glu Glu Ala Ile Phe Ser Lys Tyr Val Gly Asn Lys Ile Thr Glu
 50 55 60

Val Asp Glu Tyr Met Lys Glu Ala Val Asp His Tyr Ala Gly Gln Leu
 65 70 75 80

Met Ser Leu Asp Ile Asn Thr Glu Gln Met Cys Leu Glu Asp Ala Met
 85 90 95

Tyr Gly Thr Asp Gly Leu Glu Ala Leu Asp Leu Ser Thr Ser Ala Gly
 100 105 110

Tyr Pro Tyr Val Ala Met Gly Lys Lys Lys Arg Asp Ile Leu Asn Lys
 115 120 125

Gln Thr Arg Asp Thr Lys Glu Met Gln Lys Leu Leu Asp Thr Tyr Gly
 130 135 140

Ile Asn Leu Pro Leu Val Thr Tyr Val Lys Asp Glu Leu Arg Ser Lys
 145 150 155 160

Thr Lys Val Glu Gln Gly Lys Ser Arg Leu Ile Glu Ala Ser Ser Gly
 165 170 175

Lys Ser Arg Leu Ile Glu Ala Ser Ser Asn Asp Ser Val Ala Met Arg
 180 185 190

Met Ala Phe Gly Asn Leu Tyr Ala Ala Phe His Lys Asn Pro Gly Val
 195 200 205

Ile Thr Gly Ser Ala Val Gly Cys Asp Pro Asp Leu Phe Trp Ser Lys
 210 215 220

Ile Pro Val Leu Met Glu Glu Lys Leu Phe Ala Phe Asp Tyr Thr Gly
 225 230 235 240

Tyr Asp Ala Ser Leu Ser Pro Ala Trp Phe Glu Ala Leu Lys Met Val
 245 250 255

Leu Glu Lys Ile Gly Phe Gly Asp Arg Val Asp Tyr Ile Asp Tyr Leu
 260 265 270

Asn His Ser His His Leu Tyr Lys Asn Lys Thr Tyr Cys Val Lys Gly
 275 280 285

Gly Met Pro Ser Gly Cys Ser Gly Thr Ser Ile Phe Asn Ser Met Ile
 290 295 300

Asn Asn Leu Ile Ile Arg Thr Leu Leu Leu Lys Thr Tyr Lys Gly Ile
 305 310 315 320

Asp Leu Asp His Leu Lys Met Ile Ala Tyr Gly Asp Asp Val Ile Ala
 325 330 335

Ser Tyr Pro His Glu Val Asp Ala Ser Leu Leu Ala Gln Ser Gly Lys
 340 345 350

Asp Tyr Gly Leu Thr Met Thr Pro Ala Asp Lys Ser Ala Thr Phe Glu
355 360 365

Thr Val Thr Trp Glu Asn Val Thr Phe Leu Lys Arg Phe Phe Arg Ala
370 375 380

Asp Glu Lys Tyr Pro Phe Leu Ile His Pro Val Met Pro Met Lys Glu
385 390 395 400

Ile His Glu Ser Ile Arg Trp Thr Lys Asp Pro Arg Asn Thr Gln Asp
405 410 415

His Val Arg Ser Leu Cys Leu Leu Ala Trp His Asn Gly Glu Glu Glu
420 425 430

Tyr Asn Lys Phe Leu Ala Lys Ile Arg Ser Val Pro Ile Gly Arg Ala
435 440 445

Leu Leu Leu Pro Glu Tyr Ser Thr Leu Tyr Arg Arg Trp Leu Asp Ser
450 455 460

Phe
465

<210> 28
<211> 320
<212> PRT
<213> Human immunodeficiency virus

<400> 28
Lys Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys Pro Gly Met
1 5 10 15

Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys
20 25 30

Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser
35 40 45

Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu
 65 70 75 80

Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His
85 90 95

Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly
 100 105 110

Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr
 115 120 125
 Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr
 130 135 140
 Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe
 145 150 155 160
 Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro
 165 170 175
 Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp
 180 185 190
 Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg Gln His
 195 200 205
 Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu
 210 215 220
 Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr
 225 230 235 240
 Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp
 245 250 255
 Ile Cys Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Pro
 260 265 270
 Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys Ala
 275 280 285
 Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala
 290 295 300
 Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr Tyr Asp
 305 310 315 320